

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/963,766

CRF Processing Date: 2/17/2022
Edited by: JK
Verified by: JK (STIC staff)

- Changed a file from non-ASCII to ASCII
- Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- Edited a format error in the Current Application Data section, specifically:

- Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____
- Added the mandatory heading and subheadings for "Current Application Data".
- Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- Changed the spelling of a mandatory field (the headings or subheadings), specifically:

- Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

- Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

- Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- Inserted colons after headings/subheadings. Headings edited included:

- Deleted extra, invalid, headings used by an applicant, specifically:

- Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file;
 page numbers throughout text; other invalid text, such as _____
- Inserted mandatory headings, specifically:

- Corrected an obvious error in the response, specifically:

- Edited identifiers where upper case is used but lower case is required, or vice versa.
- Corrected an error in the Number of Sequences field, specifically:

- A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

- Other:

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/963,766

DATE: 02/17/2002
 TIME: 16:10:19

Input Set : A:\PTO.AMC.TXT
 Output Set: N:\CRF3\02172002\I963766.raw

4 <110> APPLICANT: Nakamura, Takao
 5 Ohta, Masataka
 7 <120> TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
 8 BINDING PROTEIN-COUPLED RECEPTOR PROTEIN, BG3
 11 <130> FILE REFERENCE: 06501-087001
 13 <140> CURRENT APPLICATION NUMBER: 09/963,766
 14 <141> CURRENT FILING DATE: 2001-09-25
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP00/01826
 17 <151> PRIOR FILING DATE: 2000-03-24
 19 <150> PRIOR APPLICATION NUMBER: JP 11/82641
 20 <151> PRIOR FILING DATE: 1999-03-25
 22 <160> NUMBER OF SEQ ID NOS: 6
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 21
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: Artificially synthesized primer sequence
 36 <221> NAME/KEY: misc_feature
 37 <222> LOCATION: 4
 38 <223> OTHER INFORMATION: n = a, g, c, or t
 40 <400> SEQUENCE: 1
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 43 <210> SEQ ID NO: 2
 44 <211> LENGTH: 3117
 45 <212> TYPE: DNA
 46 <213> ORGANISM: Homo sapiens
 48 <400> SEQUENCE: 2
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 50 gccgtgctgt cctccgttag caccatccgg aaccagcgct accacatcca cgccaacctg 120
 51 tccttcggcc tgctggggc ccaggctctg ctgctcatta gtttccgcct cgagccgggc 180
 52 acgaccccct gccaagtgtat ggccgtgctc ctacactact tcttcctgag tgccttcgca 240
 53 tggatgctgg tggagggggct gcacctctac agcatggtga tcaaggcttt tgggtcggag 300
 54 gacagcaaggc accgttacta ctatggatg ggatggggtt ttccctttt gatgtgcattc 360
 55 atttcaactgt catttgcatt ggacagttac ggaacaagca acaattgttg gctgtcggtt 420
 56 gcgagtggcg ccatctgggc ctttgttagcc cctgccctgt ttgtcatcgat ggtcaacattt 480
 57 ggcatacctca tcgctgtgac cagagtcatc tcacagatca ggcggcacaatc ctacaagatc 540
 58 catggagacc ccagtgccctt caagttgacg gccaaggcag tggccgtgct gctgcccattc 600
 59 ctgggtacct cgtgggtctt tggcgtgctt gctgtcaacg gttgtctgtt ggtttccatc 660
 60 tacatgttttgc ccacgctcaa ctccctgcag ggactgttca tattcctttt tcattgtctc 720
 61 ctgaatttcag aggtgagagc cgccttcaag cacaaaacca aggtctggtc gctcacgagc 780
 62 agctccggcc gcaccccttcaaa cgcgaagcccc ttccactcggtt acctcatgaa tgggacccgg 840

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/963,766

DATE: 02/17/2002
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Input Set : A:\PTO.AMC.TXT
Output Set: N:\CRF3\02172002\I963766.raw

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65	acacccccc aaacagaatg aaatgcccc ccttgccta tggaccctct ccttgctgt	1020
66	gtctggacat gggtgtgtg gccccgagac agctgtcctc ccctgtgact ctggctgtcg	1080
67	gagcacactg ctcagcccg cagcctgatg cccaggccag cgtggccct cctgccttgc	1140
68	atccacccgt gggctgagtg acttcctcg gggattccca ggacacagtgc ctgtgactgt	1200
69	gatgggtgcc ttgagcctcc cttcatcact cagcatcaga cccagcgagg ccaggacact	1260
70	cggggccggc cccgcacac caggagggga tggcagccct ctgtgccttgc tggggcttg	1320
71	gggactcagg gccaaagagg tggtcaggt cccacgcac cctcagtca ggcgaggcag	1380
72	ctgggggtgt gtgggaaaga gcatgcggag tccccagtgt ctgaatccac tgagtggta	1440
73	gttccccaca gccggcgcta gctgggtgtgt gtctctgtgt gtgggccgg cgtggccaa	1500
74	cctgtgtgtgt gtcatcagtt gggggccct gcccaagccg agctcgagcc gtggcgggg	1560
75	gtcggtgact ctccaggtga gggcgacccc tctgcctgt cttgggggg gtcccccctg	1620
76	ctcacgtgaa gagccgctct gggcctttag gctgcctgtat ggtgcctgtgt cttggggag	1680
77	cttctcgcc atccgtgtg agtttgcct ctttgaccc caattcgcc ttaagatgcc	1740
78	ctcctccctc gtgtgccagc ctccttgggt gttcttggc cacaggagct ggcgtgtcc	1800
79	cccgagtgcc tgggttccag gtggaaagtg gagggcattt tccagggcac tgcttcccc	1860
80	agaggcttcc tcatggctca caggcactct acgaagtttca taatggcag accacgcggc	1920
81	aggttagcaca gtgcgtcccg tctggtcacc atgagaccga cctgcgtca gtccccactg	1980
82	acctggagag ggagggctgg tgacagccgt gtctctgtgt ttgagggaaa tttatggact	2040
83	cagattcagc cccagaggag atggataat tggatggac ccatgtgtgg gcatgatcct	2100
84	gtggAACACA ggTTGGGAT catagatgtg aattaagaca ccaccgagat acggcgtgtg	2160
85	agttcatac tggctgata gcaactgtgg tggctgtgaa atgtggtaa gacattcaaa	2220
86	cctggttttg atactggaaa ctcttcctt aaaactgtga ccatgatttca attcagcccc	2280
87	tccacacccc tatgtctgcc ttgtttcaga gtgagtttc tatggagcct gtggccctt	2340
88	tgcagcccac ctggggctt cttaatgtaa ctctccctt ggtgcctgg agtggaccac	2400
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90	gaacctttgc tcttctgtca ggcgaggccc aggctgcacc agccacactgc cacatggta	2520
91	cagtgcacg ggcctgcgt atggccctgt caaccgtct ctggcggca cacctggctg	2580
92	ctgcaggcca aggccgtgt tcagtgaaga gtcccatgtt tagtatggac taaagtccca	2640
93	tgttttagcca ctgccccagg ctccctgtac cccagaaacc aggtcacatg gaccacagt	2700
94	ccagatcctc atcacgcgg tgagcaccta gaagtggaa cactgtatttct ctacaatgt	2760
95	cacttggata tttctctta tttagttct agtggaaacaa atcaagtaag gaactatctt	2820
96	tagtttagat ggaatttattt gtttttaattt gttggctat tcatctataat agctaataatt	2880
97	tcaagataag taatgaacaa aacctgtcta aacctttgt ttccaatgaa tgaaagtcat	2940
98	gcactttatt tatagctct atgttttgc ttctgcagta cttttattat ctatacataaa	3000
99	tttggccaaa aataagaaat tggaaagaat gaaatgttta gtttatagta gaagaaagat	3060
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105	<213> ORGANISM: Artificial Sequence	
107	<220> FEATURE:	
108	<223> OTHER INFORMATION: Artificially synthesized primer sequence	
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116	<211> LENGTH: 21	
117	<212> TYPE: DNA	

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118 <213> ORGANISM: Artificial Sequence
 120 <220> FEATURE:
 121 <223> OTHER INFORMATION: Artificially synthesized primer sequence
 125 <400> SEQUENCE: 4 21
 126 ctgctcgtga gcgaccagac c
 128 <210> SEQ ID NO: 5
 129 <211> LENGTH: 5340
 130 <212> TYPE: DNA
 131 <213> ORGANISM: Homo sapiens
 133 <220> FEATURE:
 134 <221> NAME/KEY: CDS
 135 <222> LOCATION: (517)...(3138)
 137 <400> SEQUENCE: 5
 138 ttgagccaga ccagaaggag ctcgagagcg gccgcaggac aagcccgagg agcaggcggg 60
 139 cgctccaggg gaaaaccacg cacaaaacct tcttcagaga aaagggaagc tccaaacctg 120
 140 actgagacaa acggaggctc ttgaaataaa aagaaaatac cgcaggacaa acagcctccc 180
 141 gtccccgggc gcaggtcgcg gtcacagtgg tgacctggga ttgctttccc aggactgcga 240
 142 gtcggggttg gtttctcct ccctgcattc cacagctgct ctggtcatcg caacgtgtt 300
 143 attgatcaact gaagaatctc aagtttgag acgaggaaga aacaccatt aggtctccaa 360
 144 gacagctgtg tttcacaaac ttttagggaga cagaaaatttt ctcccctgga acctgtgaaa 420
 145 atgtcccttt tccaaggaag tgaaggtaa gaggtcccggt tctcacagac cctcagtaat 480
 146 ttcacttggc tccgagctt gacctccgag agagcc atg gaa aag ctg ctg cgg 534
 147 Met Glu Lys Leu Leu Arg
 148 1 5
 150 ctg tgc tgc tgg tac tcc tgg ctg ctg cta ttt tat tac aac ttt cag 582
 151 Leu Cys Cys Trp Tyr Ser Trp Leu Leu Phe Tyr Tyr Asn Phe Gln
 152 10 15 20
 154 gtg cgt ggc gtc tac tcc aga tcg cag gac cat cca gga ttt cag gtg 630
 155 Val Arg Gly Val Tyr Ser Arg Ser Gln Asp His Pro Gly Phe Gln Val
 156 25 30 35
 158 ttg gcg tct gct tcc cat tac tgg cca ctg gag aat gtg gat ggg atc 678
 159 Leu Ala Ser Ala Ser His Tyr Trp Pro Leu Glu Asn Val Asp Gly Ile
 160 40 45 50
 162 cat gaa ctt cag gat aca act gga gat att gtg gaa ggg aag gtc aac 726
 163 His Glu Leu Gln Asp Thr Thr Gly Asp Ile Val Glu Gly Lys Val Asn
 164 55 60 65 70
 166 aaa ggc att tac ctg aaa gag gaa aag gga gtc acg ctt ctc tat tac 774
 167 Lys Gly Ile Tyr Leu Lys Glu Glu Lys Gly Val Thr Leu Tyr Tyr
 168 75 80 85
 170 ggc agg tac aac agc tcc tgc atc agc aag cca gag cag tgt ggc cct 822
 171 Gly Arg Tyr Asn Ser Ser Cys Ile Ser Lys Pro Glu Gln Cys Gly Pro
 172 90 95 100
 174 gaa ggg gtc acg ttt tct ttc tgg aag aca caa gga gaa cag tct 870
 175 Glu Gly Val Thr Phe Ser Phe Phe Trp Lys Thr Gln Gly Glu Gln Ser
 176 105 110 115
 178 aga cca atc cct tct gcg tat ggg gga cag gtc atc tcc aat ggg ttc 918
 179 Arg Pro Ile Pro Ser Ala Tyr Gly Gly Gln Val Ile Ser Asn Gly Phe
 180 120 125 130
 182 aaa gtc tgc tcc agc ggt ggc aga ggc tct gtg gag ctg tac acg cgg 966

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183	Lys Val Cys Ser Ser Gly Gly Arg Gly Ser Val Glu Leu Tyr Thr Arg		
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186	gac aat tcc atg aca tgg gag gcc tcc ttc agc ccc cca ggc ccc tat	1014	
187	Asp Asn Ser Met Thr Trp Glu Ala Ser Phe Ser Pro Pro Gly Pro Tyr		
188	155	160	165
190	tgg act cat gtc cta ttt aca tgg aaa tcc aag gag ggc ctg aaa gtc	1062	
191	Trp Thr His Val Leu Phe Thr Trp Lys Ser Lys Glu Gly Leu Lys Val		
192	170	175	180
194	tac gtc aac ggg acc ctg agc acc tct gat ccg agt gga aaa gtg tct	1110	
195	Tyr Val Asn Gly Thr Leu Ser Thr Ser Asp Pro Ser Gly Lys Val Ser		
196	185	190	195
198	cgt gac tat gga gag tcc aac gtc aac ctc gtg ata ggg tct gag cag	1158	
199	Arg Asp Tyr Gly Glu Ser Asn Val Asn Leu Val Ile Gly Ser Glu Gln		
200	200	205	210
202	gac cag gcc aag tgt tat gag aac ggt gct ttc gat gag ttc atc atc	1206	
203	Asp Gln Ala Lys Cys Tyr Glu Asn Gly Ala Phe Asp Glu Phe Ile Ile		
204 215	220	225	230
206	tgg gag cgg gct ctg act ccg gat gag atc gcc atg tac ttc act gct	1254	
207	Trp Glu Arg Ala Leu Thr Pro Asp Glu Ile Ala Met Tyr Phe Thr Ala		
208	235	240	245
210	gcc att gga aag cat gct tta ttg tct tca acg ctg cca agc ctc ttc	1302	
211	Ala Ile Gly Lys His Ala Leu Leu Ser Ser Thr Leu Pro Ser Leu Phe		
212	250	255	260
214	atg aca tcc aca gca agc ccc gtg atg ccc aca gat gcc tac cat ccc	1350	
215	Met Thr Ser Thr Ala Ser Pro Val Met Pro Thr Asp Ala Tyr His Pro		
216	265	270	275
218	atc ata acc aac ctg aca gaa gag aga aaa acc ttc caa agt ccc gga	1398	
219	Ile Ile Thr Asn Leu Thr Glu Glu Arg Lys Thr Phe Gln Ser Pro Gly		
220	280	285	290
222	gtg ata ctg agt tac ctc caa aat gta tcc ctc agc tta ccc agt aag	1446	
223	Val Ile Leu Ser Tyr Leu Gln Asn Val Ser Leu Ser Leu Pro Ser Lys		
224 295	300	305	310
226	tcc ctc tcg gag cag aca gcc ttg aat ctc acc aag acc ttc tta aaa	1494	
227	Ser Leu Ser Glu Gln Thr Ala Leu Asn Leu Thr Lys Thr Phe Leu Lys		
228	315	320	325
230	gcc gtg gga gag atc ctt cta ctg cct ggt tgg att gct ctg tca gag	1542	
231	Ala Val Gly Glu Ile Leu Leu Leu Pro Gly Trp Ile Ala Leu Ser Glu		
232	330	335	340
234	gac agc gcc gtg gta ctg agt ctc atc gac act att gac acc gtc atg	1590	
235	Asp Ser Ala Val Val Leu Ser Leu Ile Asp Thr Ile Asp Thr Val Met		
236	345	350	355
238	ggc cat gta tcc tcc aac ctg cac ggc agc acg ccc cag gtc acc gtg	1638	
239	Gly His Val Ser Ser Asn Leu His Gly Ser Thr Pro Gln Val Thr Val		
240	360	365	370
242	gag ggc tcc tct gcc atg gca gag ttt tcc gtg gcc aaa atc ctg ccc	1686	
243	Glu Gly Ser Ser Ala Met Ala Glu Phe Ser Val Ala Lys Ile Leu Pro		
244 375	380	385	390
246	aag acc gtg aat tcc tcc cat tac cgc ttc ccg gcc cac ggg cag agc	1734	
247	Lys Thr Val Asn Ser Ser His Tyr Arg Phe Pro Ala His Gly Gln Ser		

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Input Set : A:\PTO.AMC.TXT
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248	395	400	405	
250	ttc atc cag atc ccc cac gag gcc ttc cac agg cac gcc tgg agc acc			1782
251	Phe Ile Gln Ile Pro His Glu Ala Phe His Arg His Ala Trp Ser Thr			
252	410	415	420	
254	gtc gtg ggt ctg ctg tac cac agc atg cac tac tac ctg aac aac atc			1830
255	Val Val Gly Leu Leu Tyr His Ser Met His Tyr Tyr Leu Asn Asn Ile			
256	425	430	435	
258	tgg ccc gcc cac acc aag atc gcg gag gcc atg cat cac cag gac tgc			1878
259	Trp Pro Ala His Thr Lys Ile Ala Glu Ala Met His His Gln Asp Cys			
260	440	445	450	
262	ctg ctg ttc gcc acc agc cac ctg att tcc ctg gag gtg tcc cca cca			1926
263	Leu Leu Phe Ala Thr Ser His Leu Ile Ser Leu Glu Val Ser Pro Pro			
264	455	460	465	470
266	ccc acc ctg tct cag aac ctg tcg ggc tct cca ctc att acg gtc cac			1974
267	Pro Thr Leu Ser Gln Asn Leu Ser Gly Ser Pro Leu Ile Thr Val His			
268	475	480	485	
270	ctc aag cac aga ttg aca cgt aag cag cac agt gag gcc acc aac agc			2022
271	Leu Lys His Arg Leu Thr Arg Lys Gln His Ser Glu Ala Thr Asn Ser			
272	490	495	500	
274	agc aac cga gtc ttc gtg tac tgc gcc ttc ctg gac ttc agc tcc gga			2070
275	Ser Asn Arg Val Phe Val Tyr Cys Ala Phe Leu Asp Phe Ser Ser Gly			
276	505	510	515	
278	gaa ggg gtc tgg tcg aac cac ggc tgt gcg ctc acg aga gga aac ctc			2118
279	Glu Gly Val Trp Ser Asn His Gly Cys Ala Leu Thr Arg Gly Asn Leu			
280	520	525	530	
282	acc tac tcc gtc tgc cgc tgc act cac ctc acc aac ttt gcc atc ctc			2166
283	Thr Tyr Ser Val Cys Arg Cys Thr His Leu Thr Asn Phe Ala Ile Leu			
284	535	540	545	550
286	atg cag gtg gtc ccg ctg gag ctt gca cgc gga cac cag gtg gcg ctg			2214
287	Met Gln Val Val Pro Leu Glu Leu Ala Arg Gly His Gln Val Ala Leu			
288	555	560	565	
290	tcg tct atc agc tat gtg ggc tgc tcc ctc tcc gtg ctc tgc ctg gtg			2262
291	Ser Ser Ile Ser Tyr Val Gly Cys Ser Leu Ser Val Leu Cys Leu Val			
292	570	575	580	
294	gcc acg ctg gtc acc ttc gcc gtg ctg tcc tcc gtg agc acc atc cgg			2310
295	Ala Thr Leu Val Thr Phe Ala Val Leu Ser Ser Val Ser Thr Ile Arg			
296	585	590	595	
298	aac cag cgc tac cac atc cac gcc aac ctg tcc ttc gcc gtg ctg gtg			2358
299	Asn Gln Arg Tyr His Ile His Ala Asn Leu Ser Phe Ala Val Leu Val			
300	600	605	610	
302	gcc cag gtc ctg ctg ctc att agt ttc cgc ctc gag ccg ggc acg acc			2406
303	Ala Gln Val Leu Leu Ile Ser Phe Arg Leu Glu Pro Gly Thr Thr			
304	615	620	625	630
306	ccc tgc caa gtg atg gcc gtg ctc cta cac tac ttc ttc ctg agt gcc			2454
307	Pro Cys Gln Val Met Ala Val Leu Leu His Tyr Phe Phe Leu Ser Ala			
308	635	640	645	
310	ttc gca tgg atg ctg gtg gag ggg ctg cac ctc tac agc atg gtg atc			2502
311	Phe Ala Trp Met Leu Val Glu Gly Leu His Leu Tyr Ser Met Val Ile			
312	650	655	660	

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/963,766

DATE: 02/17/2002
TIME: 16:10:21

Input Set : A:\PTO.AMC.TXT
Output Set: N:\CRF3\02172002\I963766.raw

L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/963,766

DATE: 02/08/2002
TIME: 11:39:39

Input Set : A:\06501-087001.TXT
Output Set: N:\CRF3\02082002\I963766.raw

Joes N. Comph
Dept. of P. & I. atte Nevada

4 <110> APPLICANT: Nakamura, Takao
5 Ohta, Masataka
7 <120> TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
8 BINDING PROTEIN-COUPLED RECEPTOR PROTEIN, BG3
11 <130> FILE REFERENCE: 06501-087001
13 <140> CURRENT APPLICATION NUMBER: 09/963,766
14 <141> CURRENT FILING DATE: 2001-09-25
16 <150> PRIOR APPLICATION NUMBER: PCT/JP00/01826
17 <151> PRIOR FILING DATE: 2000-03-24
19 <150> PRIOR APPLICATION NUMBER: JP 11/82641
20 <151> PRIOR FILING DATE: 1999-03-25
22 <160> NUMBER OF SEQ ID NOS: 6
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

408 <210> SEQ ID NO: 6
409 <211> LENGTH: 874
410 <212> TYPE: PRT
411 <213> ORGANISM: Homo sapiens
413 <400> SEQUENCE: 6
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415 1 5 10 15
416 Phe Tyr Tyr Asn Phe Gln Val Arg Gly Val Tyr Ser Arg Ser Gln Asp
417 20 25 30
418 His Pro Gly Phe Gln Val Leu Ala Ser Ala Ser His Tyr Trp Pro Leu
419 35 40 45
420 Glu Asn Val Asp Gly Ile His Glu Leu Gln Asp Thr Thr Gly Asp Ile
421 50 55 60
422 Val Glu Gly Lys Val Asn Lys Gly Ile Tyr Leu Lys Glu Glu Lys Gly
423 65 70 75 80
424 Val Thr Leu Leu Tyr Tyr Gly Arg Tyr Asn Ser Ser Cys Ile Ser Lys
425 85 90 95
426 Pro Glu Gln Cys Gly Pro Glu Gly Val Thr Phe Ser Phe Phe Trp Lys
427 100 105 110
428 Thr Gln Gly Glu Gln Ser Arg Pro Ile Pro Ser Ala Tyr Gly Gly Gln
429 115 120 125
430 Val Ile Ser Asn Gly Phe Lys Val Cys Ser Ser Gly Gly Arg Gly Ser
431 130 135 140
432 Val Glu Leu Tyr Thr Arg Asp Asn Ser Met Thr Trp Glu Ala Ser Phe
433 145 150 155 160
434 Ser Pro Pro Gly Pro Tyr Trp Thr His Val Leu Phe Thr Trp Lys Ser

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Input Set : A:\06501-087001.TXT

Output Set: N:\CRF3\02082002\I963766.raw

435	165	170	175
436	Lys Glu Gly Leu Lys Val Tyr Val Asn Gly Thr Leu Ser Thr Ser Asp		
437	180	185	190
438	Pro Ser Gly Lys Val Ser Arg Asp Tyr Gly Glu Ser Asn Val Asn Leu		
439	195	200	205
440	Val Ile Gly Ser Glu Gln Asp Gln Ala Lys Cys Tyr Glu Asn Gly Ala		
441	210	215	220
442	Phe Asp Glu Phe Ile Ile Trp Glu Arg Ala Leu Thr Pro Asp Glu Ile		
443	225	230	235
444	Ala Met Tyr Phe Thr Ala Ala Ile Gly Lys His Ala Leu Leu Ser Ser		
445	245	250	255
446	Thr Leu Pro Ser Leu Phe Met Thr Ser Thr Ala Ser Pro Val Met Pro		
447	260	265	270
448	Thr Asp Ala Tyr His Pro Ile Ile Thr Asn Leu Thr Glu Glu Arg Lys		
449	275	280	285
450	Thr Phe Gln Ser Pro Gly Val Ile Leu Ser Tyr Leu Gln Asn Val Ser		
451	290	295	300
452	Leu Ser Leu Pro Ser Lys Ser Leu Ser Glu Gln Thr Ala Leu Asn Leu		
453	305	310	315
454	320		
455	Thr Lys Thr Phe Leu Lys Ala Val Gly Glu Ile Leu Leu Leu Pro Gly		
456	325	330	335
457	Trp Ile Ala Leu Ser Glu Asp Ser Ala Val Val Leu Ser Leu Ile Asp		
458	340	345	350
459	Thr Ile Asp Thr Val Met Gly His Val Ser Ser Asn Leu His Gly Ser		
460	355	360	365
461	Thr Pro Gln Val Thr Val Glu Gly Ser Ser Ala Met Ala Glu Phe Ser		
462	370	375	380
463	Val Ala Lys Ile Leu Pro Lys Thr Val Asn Ser Ser His Tyr Arg Phe		
464	385	390	395
465	400		
466	Pro Ala His Gly Gln Ser Phe Ile Gln Ile Pro His Glu Ala Phe His		
467	405	410	415
468	Arg His Ala Trp Ser Thr Val Val Gly Leu Leu Tyr His Ser Met His		
469	420	425	430
470	Tyr Tyr Leu Asn Asn Ile Trp Pro Ala His Thr Lys Ile Ala Glu Ala		
471	435	440	445
472	Met His His Gln Asp Cys Leu Leu Phe Ala Thr Ser His Leu Ile Ser		
473	450	455	460
474	Leu Glu Val Ser Pro Pro Thr Leu Ser Gln Asn Leu Ser Gly Ser		
475	465	470	475
476	480		
477	Pro Leu Ile Thr Val His Leu Lys His Arg Leu Thr Arg Lys Gln His		
478	485	490	495
479	Ser Glu Ala Thr Asn Ser Ser Asn Arg Val Phe Val Tyr Cys Ala Phe		
480	500	505	510
481	Leu Asp Phe Ser Ser Gly Glu Gly Val Trp Ser Asn His Gly Cys Ala		
482	515	520	525
483	Leu Thr Arg Gly Asn Leu Thr Tyr Ser Val Cys Arg Cys Thr His Leu		
530	535	540	
545	Thr Asn Phe Ala Ile Leu Met Gln Val Val Pro Leu Glu Leu Ala Arg		
550	555	560	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/963,766

DATE: 03/03/2002

TIME: 11:39:39

Input Set : A:\06501-087001.TXT

Output Set: N:\CRF3\02082002\I963766.raw

484 Gly His Gln Val Ala Leu Ser Ser Ile Ser Tyr Val Gly Cys Ser Leu
 485 565 570 575
 486 Ser Val Leu Cys Leu Val Ala Thr Leu Val Thr Phe Ala Val Leu Ser
 487 580 585 590
 488 Ser Val Ser Thr Ile Arg Asn Gln Arg Tyr His Ile His Ala Asn Leu
 489 595 600 605
 490 Ser Phe Ala Val Leu Val Ala Gln Val Leu Leu Leu Ile Ser Phe Arg
 491 610 615 620
 492 Leu Glu Pro Gly Thr Thr Pro Cys Gln Val Met Ala Val Leu Leu His
 493 625 630 635 640
 494 Tyr Phe Phe Leu Ser Ala Phe Ala Trp Met Leu Val Glu Gly Leu His
 495 645 650 655
 496 Leu Tyr Ser Met Val Ile Lys Val Phe Gly Ser Glu Asp Ser Lys His
 497 660 665 670
 498 Arg Tyr Tyr Tyr Gly Met Gly Trp Gly Phe Pro Leu Leu Ile Cys Ile
 499 675 680 685
 500 Ile Ser Leu Ser Phe Ala Met Asp Ser Tyr Gly Thr Ser Asn Asn Cys
 501 690 695 700
 502 Trp Leu Ser Leu Ala Ser Gly Ala Ile Trp Ala Phe Val Ala Pro Ala
 503 705 710 715 720
 504 Leu Phe Val Ile Val Val Asn Ile Gly Ile Leu Ile Ala Val Thr Arg
 505 725 730 735
 506 Val Ile Ser Gln Ile Ser Ala Asp Asn Tyr Lys Ile His Gly Asp Pro
 507 740 745 750
 508 Ser Ala Phe Lys Leu Thr Ala Lys Ala Val Ala Val Leu Leu Pro Ile
 509 755 760 765
 510 Leu Gly Thr Ser Trp Val Phe Gly Val Leu Ala Val Asn Gly Cys Ala
 511 770 775 780
 512 Val Val Phe Gln Tyr Met Phe Ala Thr Leu Asn Ser Leu Gln Gly Leu
 513 785 790 795 800
 514 Phe Ile Phe Leu Phe His Cys Leu Leu Asn Ser Glu Val Arg Ala Ala
 515 805 810 815
 516 Phe Lys His Lys Thr Lys Val Trp Ser Leu Thr Ser Ser Ser Ala Arg
 517 820 825 830
 518 Thr Ser Asn Ala Lys Pro Phe His Ser Asp Leu Met Asn Gly Thr Arg
 519 835 840 845
 520 Pro Gly Met Ala Ser Thr Lys Leu Ser Pro Trp Asp Lys Ser Ser His
 521 850 855 860
 522 Ser Ala His Arg Val Asp Leu Ser Ala Val
 523 865 870

E--> 527(7)

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/963,766

DATE: 02/08/2002

TIME: 11:39:40

Input Set : A:\06501-087001.TXT

Output Set: N:\CRF3\02082002\I963766.raw

L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:527 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6